

Whitefly-Transmitted Viruses Threatening Tomato Production in Oman

Q. M. I. Haq¹, I. S. Al Amri², A. S. F. Al Harrasi³, A. S. S. A. Wadair⁴

¹ Associate Professor, Department of Biological Sciences and Chemistry, College of Arts and Sciences, University of Nizwa, Oman. quaziimran@unizwa.edu.om

² Associate Professor, Department of Biological Sciences and Chemistry, College of Arts and Sciences, University of Nizwa, Oman. issa.alamri@unizwa.edu.om

Professor, Chair of Oman Medicinal Plants and Marine Products, University of Nizwa, Oman. aharrasi@unizwa.edu.om

Laboratory Specialist and Consultant, General Directorate of Veterinary Services, Royal Court Affairs, Muscat, Oman. aliawladwadair@unizwa.edu.om

Abstract: Tomato (*Solanum lycopersicum*) is a vital crop in Oman, contributing significantly to the country's agricultural economy and food security. However, the tomato industry faces a critical threat from whitefly-transmitted viruses that have emerged as a major concern for tomato growers in the region. This abstract summarizes the pressing issue of whitefly-transmitted viruses and their impact on tomato production in Oman. Whiteflies (*Bemisia tabaci*), small sap-feeding insects, have become notorious for their role in transmitting various devastating viruses to tomato plants. These viruses, including *Tomato yellow leaf curl virus* (TYLCV), *Tomato leaf curl virus* (ToLCV), and *Tomato chlorosis virus* (ToCV), can cause severe damage to tomato crops, leading to reduced yields, poor fruit quality, and substantial economic losses for farmers.

This abstract emphasizes the urgent need for a comprehensive approach to mitigate the impact of whitefly-transmitted viruses on tomato production in Oman. Such an approach may include integrated pest management strategies, breeding programs for resistant tomato varieties, and education and awareness campaigns for farmers. Additionally, collaborative efforts between researchers, farmers, and policymakers are essential to develop sustainable solutions and ensure the continued viability of the tomato industry in Oman. Whitefly-transmitted viruses pose a significant threat to tomato production in Oman, jeopardizing food security and economic stability. Addressing this issue requires immediate attention and a concerted effort to protect the tomato industry, safeguard livelihoods, and ensure a sustainable future for agriculture in the country.

Keywords: Tomato, Whiteflies, Tomato Leaf Curl Diseases (TLCDs), Production, Resistant

1. INTRODUCTION

Two whiteflies (Hemiptera: Aleyrodidae) transmitted viral disease complexes, Tomato Leaf Curl Diseases (TLCDs) and Tomato Yellow Leaf Curl Diseases (TYLCDs), are the primary threats to tomato production across Oman [Jacobson et al., 2018; Patil et al. 2016]. Tomato production reached 201 kt in 2019 in Oman, according to Faostat. This is 1.03% more than in the previous year. Historically, tomato production in Oman reached an all-time high of 201 kt in 2019 and an all-time low of 0.100 kt in 1977, according to Faostat. Oman has been ranked 64th among the 152 countries we follow in terms of interest rates on tomato production. It is an easy crop to grow, making it a staple food for nearly one billion people in the tropics, sub-tropics, and Middle East [Leg et al., 2015]. While tomato production is sometimes affected by viral diseases worldwide [Leg et al., 2015], in the Middle East, these viruses are a persistent and emergent threat to food security, causing losses of over US\$ 1 billion annually [Jacobson et al., 2018; Leg et al., 2015, Manyong et al., 2010].

In value terms, tomato production declined to \$X in 2021, estimated in export price. In general, the show, however, posted a substantial increase. The growth pace was the most rapid in 2017, with a rise of X%. Tomato production

peaked at \$X in 2020 and dropped the following year. The average yield of tomatoes in Oman plummeted to X tons per ha in 2021, waning by -X% compared with the previous year. Over the period under review, the yield, however, recorded a relatively flat trend pattern. The most prominent growth rate was recorded in 2017 when the product increased by X% against the previous year. The tomato yield peaked at X tons per ha in 2019; from 2020 to 2021, the result stood at a somewhat lower figure. Despite the increased use of modern agricultural techniques and methods, adverse weather conditions may still impact future yield figures. In 2021, the total area harvested for tomato production in Oman stood at X ha, surging by X% on the previous year's figure. Over the period under review, the harvested area saw resilient growth. The pace of change appeared the most rapid in 2017 when the harvested area increased by X% against the previous year. Over the period under review, the harvested site dedicated to tomato production attained the maximum in 2021 and is likely to see steady growth in years to come [<https://www.indexbox.io/store/oman-tomato-market-report-analysis-and-forecast-to-2025/>]

These Viruses Believed Herb Originated in Hospital Africa and Spread Across Te Continental by the Human-Mediated Movement of Vegetarian Promoted Kasawa Cuttings [Jacobson et al., 2018; Thresh et al., 1994] and whitefly vectors [Dubern et al., 1994; Maruthi et al., 2005; Maruthi et al., 2017; Mware et al., 2009]. Although tomato viruses have been reported in Oman for more than 15 years, severe epidemics of both TLCs and TYLCs causing viral complexes have emerged in Oman during the past 10 years that have caused famine, reduced yields, and in some regions, severely restricted tomato production. Research findings during the first decade after the emergence of the severe TLCs and TYLCs addressing disease incidence, mechanisms of spread, virus identification, vectors, management strategies, and proposed theories for the widespread occurrence of the causative virus and abundance of the vectors have been reviewed in Refs. [Jacobson et al., 2018; Legg et al., 2015; Legg et al., 2014; Macfadyen et al., 2018; Legg et al., 2011; Legg et al., 2009; Brown et al., 2010; Thompson et al., 2011; Thompson et al., 2011; Colvin et al., 2006; Legg et al., 2014]. Molecular biology tools and approaches developed over the past decade, such as Next Generation Sequencing (NGS), NextRAD sequencing, and bioinformatics tools, have enabled the identification and characterization of the genetic diversity of vectors [Boykin et al., 2018] and viral [Ateka et al., 2017] populations which have long been recognized as essential factors underlying reported variation in disease severity, vector competence [Bedford et al., 1994] and coevolution of vectors and viruses [Jacobson et al., 2018; Maruthi et al., 2002]. This review aims to provide a current synthesis of the literature on the diversity of whiteflies, tomato viruses, and their interactions across Oman.

2. WHITEFLY-TRANSMITTED VIRAL DISEASE COMPLEXES OF TOMATO

Oman has become a linkage of begomoviruses of various topographical ancestries [Khan et al., 2014]. The tendency for mixing, the primary tool for developing this virus, and the potential for transmission are increasing as Oman (and several other Arab nations) are vital centers of air and sea trade and travel [Khan et al., 2013a; Khan et al., 2013b]. This virus produces a novel, infectious strain over mixing. In Middle Eastern nations, the virus is more transmitted due to ubiquitous trade and air and sea travel. Significant income losses and socio-economic improvements require efforts to study and develop long-term strategies to combat this devastating virus to ensure sustainable and cost-effective results without the heavy use of pesticides. Leaf curl of begomovirus is the central lethal infection of many significant crops in Oman, together with tomatoes, peppers, chilies, pumpkins, melons, and cucumbers [Khan et al., 2012]. Subject to controlling applies, profit harms of these harvests can range from 0% to 100% and have been reported in Nizwa, Al Bateen, Musandam, Buraimi, Salalah, and inside Oman. Over the previous eight years, several begomoviruses have been categorized in Oman, containing numerous sparingly significant crops. Study in Oman is currently focused solely on the molecular classification of these viruses, which is only the first step towards developing strategies to control these essential plant viruses. Therefore, further research needs to be done on topics such as viral protein function, viral host interactions, resistance to viral-derived transformation, and related satellites. This chapter reviews the importance of begomoviruses for Omani agriculture, research on begomoviruses done in Oman over the previous 8 years, and possible future directions for more efficient and effective control and management of this viral disease.

So far, begomoviruses have been reported in nine crop groups in Oman. Only preliminary studies of begomoviruses, such as molecular replication, characterization, and phylogenetic analysis, have been performed [Haq and Sohrab, 2020]. In winter, tomatoes are grown on a big scale in the Albertina area of Oman. Leaves showing symptoms were collected, total nucleic acid was isolated, and the complete viral DNA was cloned and sequenced. Sequencing results

indicated it to be closely related to TYLCV-IR (an Iranian unimolecular begomovirus species) with 91% nt identity. The Omani isolate was nominated TYLCV-OM and was reflected as a TYLCV-IR isolate. The satellite DNA sequence showed 88.5% similarity to the Pakistani beta DNA molecule. It was the first statement of beta satellite DNA (sat DNA) associated with TYLCV species. Alphasatellites and related betasatellites have been described for TYLCV-Om and therefore characterize a begomovirus intricate for Asia and the Middle East [Haq and Sohrab, 2020; Khan et al., 2008]. This alpha satellite has the same 90% nucleotide identity as the unusual Ageratum Yellow Vein Singapore Alphasatellite (AYVSGA) DNA-2. Holcomb was established to contain recombinant TYLCV-OM and *Papaya leaf roll virus* (PLRV) from the Indian subcontinent. Begomovirus is a foremost danger to Omani tomato crops. The four sequences were new species named *Tomato leaf curl Albatina virus* (ToLCABV). ToLCABVise is a recombination of ChiLCV-OM and ToLCOMV [Khan et al., 2014]. Plant inoculation studies have shown that ToLCABV interacts with ToLCB in plants [Khan et al., 2013a].

Over the past 15 years, several begomoviruses were studied in Oman, including several significant crops. Recent studies in Oman have focused solely on the molecular characterization of this virus, which is only the first step in developing strategies to control this vital plant virus and its resulting resistance. Therefore, further work, such as viral protein function, molecular interactions between begomoviruses and hosts, and the natural and experimentally induced transformation resistance of viruses and related satellites, must be performed to understand molecular crosstalk better. They revealed features of their biology and new methodologies to switch and control.

The *Bemisia tabaci* whitefly taxa consist of many morphologically identical genetic variants, only a few of which, including B, have an invasive haplotype [Paredes-Montero et al., 2021]. This haplotype has reproductive potential for pest and plant-irrigated agroecosystems worldwide. Although unprecedented outbreaks associated with B variants were reported worldwide in the 1980s, the exact origin of the invasive haplotype has not been determined. The present study investigated available models for conserved single nucleotide alteration (SNP) patterns [Paredes-Montero et al., 2021]. Whitefly sequence records show North African and Middle Eastern habitats, proposed centers of origin for variant B, and remote areas recently invaded by haplotypes of variant B. Analysis revealed eight SNP groups (haplotypes,) indicating that the genetic structure of Mitotype B is more complex than previously known. Moreover, the distribution patterns of the eight B haplotypes are closely related to well-defined ecological regions, suggesting that the different groups varied through geographic isolation. Contrary to claims that variant B is collectively invasive, only two of the eight haplotype clusters were established in geographic locations outside the uniqueness domain [Paredes-Montero et al., 2021].

Begomovirus research primarily involves molecular characterization of viruses, phylogenetic investigation, infectivity in host plants, DNA replication, resistance to transformation, analysis of promoters, and expansion of vectors. Virus-based gene silencing. In this review, diseases caused by TLCV and TYLCV in tomatoes and other crops in Oman over the past 15 years have been discussed and focus on the critical areas of future research on begomoviruses that require more attention. Considering the importance of begomoviruses TLCV and TYLCV in Omani agriculture, notable scientific accomplishments associated with begomoviruses conducted in Oman over the past 15 years or so and possible directions for efforts are reviewed here.

3. WHITEFLY VECTORS OF TOMATO VIRUSES

The frequency of tomato viruses in this area is mainly caused by vector transmission, which can lead to significant infections in crop fields [Jacobson et al., 2018; Shinishevsk, etc., 2017]. TLCB and TYLCB are assigned to Tobacco Bemisia (Gennadius) [Ghosh et al., 2004], circulating and non-distributive lyric [Jacobson et al., 2018; Njoge et al., 2017]. The middleman produced by this disease is called the matchmaker disease method, and most conditions have different effects in the eastern Fuchu region.

Since the first identification of *B. tabaci* as a pest of tobacco crops in Greece [Paredes-Montero et al., 2021; Avidov, 1956], it has been increasingly recognized as an agricultural pest worldwide due to damage caused by feeding and as the vector of plant virus pathogens [Paredes-Montero et al., 2021; Brown, 1992; Bedford et al., 1994; Jones, 2003]. Large-scale agricultural crop damage by *B. tabaci* as a sporadic pest has been documented since the 1930s, particularly in cotton-vegetable cropping systems in Egypt, India, Israel, Sudan, and Central and South America [Azab et al., 1971; Horowitz et al., 1984]. In the Jordan Valley, *B. tabaci* was shown to complete up to 15 generations per year due to the favorable hot climate and 11 ages in the coastal areas [Avidov et al., 1956]. During the mid-1970s,

unprecedented outbreaks and crop damage were reported in Israel and Egypt, while another significant explosion occurred in Israel in 1988 [Paredes-Montero et al., 2021; Brown, 1992]. The mid-1990s reduced severity following the regular use of pyrethroids and other new insecticides [Gerling et al., 1986]. Among the mitotypes of historical importance are the well-known B and Q mitotypes [Paredes-Montero et al., 2021; Brown, 2010; Bayhan et al., 2006; Paredes-Montero et al., 2020; Shaurub et al., 2021], the A mitotype endemic to the American tropics and Caribbean Basin [9,22], the Asia I and II in the Indian subcontinent [Rekha et al., 2005], and sub-Saharan Africa mitotypes [Paredes-Montero et al., 2021; Legg et al., 2014].

More articles are published in Amman. Bifidobacteria are widely transmitted and intersected. Strange shapes are twisted back into shapes, and the rest of the foundations are used using silk threads; a person who claims that the group's name differs from the document due to the limitation of its content changes by the new token, that is, the example. This object is written in the name of water scattered by flight, and those that belong to the white fly accumulate at first sight. In this way, the separation of species from people is the presence of things because the water goes down, a limited number of days change, and the number varies. Also, self-determination is not a specification but has not yet been included in the whiteflybase.org, which coincides with the biography of the whiteflybase.org emperor. He was not missed but used different colors such as Zhou Wenzhi, Omani grass, and lice as cloth. In sub-Saharan Africa, in sub-Saharan Africa, not among the strips of sand, everything in society looks at the remains and species of whiteflies. Proof of its Omani origin in white color is that it can grow, as it occurs with a small bull, periods, Monteiro, etc. Brown et al. p. 22. Golden mitochondria are based on a quick preliminary study of the speed of time, so all the rates accumulated between species must deal with fundamentals, basals, and genera; the changes are significant and very uncomfortable; Castro and others have been carrying fish for a year. In white dots, the metaphor of the nuclear genome is replaced by golden strands, grains, toughness, and evenness, but due to the correlation between target fractures and high geographic scores, Ming Wei turned into a state of soft and split white spots. Marron Brown and others, it's over. Morally unique equivalent, two years. With this new information and simple analysis of pill tips from "DNA barcoding," large datasets worldwide are becoming more useful for studying large sets and populations of species. – Paredes Montero et al., 2021.

Les Romoris Lyce Derriere Annette Chang'l'Hersey à Kos de L'Aperentisace de Groupe Wong, It's Les Ansin Teles, La Mladic Anne Consicense, It's La Science de Tuts Chos Rensite, Mulberry Kom Les Ansin Teles that L'Aubergine, La Mladic Eile Malle, It Les Romors Incigente Les Intension de L'Hattie Itodite à Chuck Thornant.

Reciprocal reversal experiments and population genetics have provided evidence of gene flow and disturbances at the local, regional, and continental levels among tomato-related *B. tabaci* and subgroups [Jacobson et al., 2010] Elficia et al., 2018; However, the intensity and direction of gene flow between hypothetical species and their subgroups are variable. Genes can travel and mix over long distances through commercial media [Elfekih et al., 2018] and human fragmentation as the distribution of whiteflies. However, the geographical structure between the Tabaki species and subgroups associated with *B* tomatoes is often found in Japan and the Middle East [Tajebe et al. 2016]. In the discussion of whole gene grouping, whitefly roots form different networks, leak into all living things using silk nets, and fish can also be caught between nets and nets, producing trapped soil. Genomic transport methods have identified vector viruses [Chen et al., 2016] and economically necessary genes and gene families associated with vector virus interactions and endemic symbiosis [Serovagi et al., 2017]. All species-level symptoms, population inheritance and heterogeneity, molecular ecology, genomics, temporal stability of geographical rulers, gene flow and gene structure, and epidemiology for treating diseases carried by white spot. 2018; Fat Sula et al., 22.

Endosymbionts are an essential feature of *B. tabaci*, influencing epidemiologically significant life cycles and transmission phenotypes. They should be included in the characteristics of *B. tabaci* to determine their significance. Several studies have examined the genetic diversity of whitefly endosymbionts, their distribution in *B. tabaci* species and populations, and the effect of symbiosis on whitefly fitness, host plants, and vector phenotypes [Jacobson et al., 2010]. Seruwagi et al. The cellular compartment specializing in tobacco, the main endosymbiont/binding of *Candidatus portiar* Aleyrodidae, is necessary for synthesizing amino acids for growth and development [Jacobson et al., 2005]. Clark et al. Bauman et al., 2004; Thao et al., 2004]. Secondary/facultative endosymbionts are not required to survive but can affect fitness.

Endodomion is mainly transmitted through maternal lines [Jacobson et al., 2018; Thierry et al., 2011]. Although the underlying causes of many endoscopic profiles for *B. tabaci* are not understood, the introduction of new *B. tabaci*

species with nested hosts and gene flows can lead to the acquisition of new inner hearts. Research shows that lactation bacteria are meticulously determined and intertwined, crotch, with powder, lice species, subgroups, and species, Jacobson, Paredes Montero, et al., 22. But they need to care about using the campsite's host accommodation and planting items. Among them, a small number of homobiotic whiteflies to test the internal discussion, and the body of the cassava whitefly homobiotic it happens to hurt sexual homosexuality. You can not talk about powdered whitefly in Oman; they are all infected with this disease.

4. CONCLUSIONS

Accurate identification of different species and populations of tomato viruses and their vectors is an essential first step in understanding the vector-virus-plant-environmental interactions that are the subject of tomato virus epidemiology in Oman. [Jacobson et al., 2018]. Before the molecular identification of the study populations. The results could be drawn from something about the incidence, distribution, severity, and role of specific insects, mainly when genetic differences in habitat populations affect the interaction between pathogens, viruses, and culture among the study areas [Jacobson et al., 2018]. The main idea of the legend is characteristic; just like the previous master, the whitefly pierced his knowledge through needles, the transmission of tomato fungus, disease risk, mold removal style, and population size when teaching white fabric. Other forms noted as poisons, objects holding each other, mediating changes in the shape of the body it carries, the position of the body, the interior, and figure that live together in the cycle, the changes in the efficiency of the transmission and this mutually beneficial engine should also be investigated, reviewed in Refs. [Jacobson et al., 2018; Legg et al., 2014; Mauck et al., 2016; Wei et al., 2017]. Finally, understanding the white cassava virus's origin, distribution, and evolutionary potential will require a comprehensive approach that studies the agricultural ecosystem of tomatoes. He acknowledges that viral metapopulation in cross-section and white-collar recombination extends throughout the landscape and plant.

Acknowledgments

We are grateful to the University of Nizwa, Oman for providing a grant under the project reference Code (ID# UoN/CAS/IF/2023/12).

Competing of interest

There is no competing of interest declared.

5. REFERENCES

- [1]. Jacobson AL, Duffy S, Sseruwagi P. Whitefly-transmitted viruses threatening cassava production in Africa. *Current opinion in virology*. 2018 Dec 1;33:167-76.
- [2]. Patil BL, Legg JP, Kanju E, Fauquet CM: Cassava brown streak disease: a threat to food security in Africa. *J Gen Virol* 2015, 96:956-968.
- [3]. Legg JP, Kumar LP, Makesh Kumar T, Tripathi L, Ferguson M, Kanju E, Ntawuruhunga P, Cuellar W: Cassava Virus Diseases: Biology, Epidemiology, and Management. Elsevier Inc.; 2015.
- [4]. Manyong VM, Maeda C, Kanju E, Legg JP: Economic damages of cassava brown streak disease in sub-Saharan Africa: a framework | CCAFS: CGIAR research program on Climate Change, Agriculture and Food Security. In Proceedings of the 11th Triennial Symposium of the ISTRC-AB Held at the Memling Hotel: Tropical Roots and Tuber Crops and the Challenges of Globalization and Climate Changes. 2010:78-82.
- [5]. Thresh JM, Fishpool LDC, Otim-Nape GW, Fargettey D: African cassava mosaic virus disease: an underestimated and unsolved problem. *Trop Sci* 1994, 34:3-14.
- [6]. Dubern J: Transmission of African cassava mosaic geminivirus by the whitefly (*Bemisia tabaci*). *Trop Sci* 1994, 34:82-91. 10.
- [7]. Maruthi MN, Hillocks RJ, Mtunda K, Raya MD, Muhanna M, Kiozia H, Rekha AR, Colvin J, Thresh JM: Transmission of Cassava brown streak virus by *Bemisia tabaci* (Gennadius). *J Phytopathol* 2005, 153:307-312. 11.
- [8]. Maruthi MN, Jeremiah SC, Mohammed IU, Legg JP: The role of the whitefly, *Bemisia tabaci* (Gennadius), and farmer practices in the spread of cassava brown streak ipomoviruses. *J Phytopathol* 2017, 165:707-717. 12.
- [9]. Mware B, Narla R, Amata R, Olubayo F, Songa J, Kyamanyua S, Ateka EM: Efficiency of cassava brown streak virus transmission by two whitefly species in coastal Kenya. *J Gen Mol Virol* 2009, 1:040-045.
- [10]. Legg JP, Shirima R, Tajebe LS, Guastella D, Boniface S, Jeremiah S, Nsami E, Chikoti P, Rapisarda C: Biology and management of *Bemisia* whitefly vectors of cassava virus pandemics in Africa. *Pest Manag Sci* 2014, 70:1446-1453.

- [11]. Macfadyen S, Paull C, Boykin LM, De Barro P, Maruthi MN, Otim M, Kalyebi A, Vassaˆo DG, Sseruwagi P, Tay WT: Cassava Whitefly, *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) in East African Farming Landscapes: A Review of the Factors Determining Abundance. 2018 <http://dx.doi.org/10.1017/S0007485318000032>.
- [12]. Legg JP, Jeremiah SC, Obiero HM, Maruthi MN, Ndyetabula I, Okao-Okuja G, Bouwmeester H, Bigirimana S, Tata-Hangy W, Gashaka G: Comparing the regional epidemiology of the cassava mosaic and cassava brown streak virus pandemics in Africa. *Virus Res* 2011, 159:161-170.
- [13]. Legg JP: Epidemiology of a whitefly-transmitted cassava mosaic geminivirus pandemic in Africa. *Bemisia: Bionomics and Management of a Global Pest*. Netherlands: Springer; 2009, 233-257.
- [14]. Brown JK: Phylogenetic biology of the *Bemisia tabaci* sibling species group. In *Bemisia: Bionomics and Management of a Global Pest*. Edited by Stansly PA, Naranjo SE. Netherlands: Springer; 2010:31-67.
- [15]. Thompson WMO: Association of *Bemisia tabaci* with the severe cassava mosaic disease in Uganda. The Whitefly, *Bemisia tabaci* (Homoptera: Aleyrodidae) Interaction with Geminivirus-Infected Host Plants. Springer Netherlands; 2011:89-105.
- [16]. Thompson WMO: Interaction of *Bemisia tabaci* with East African cassava mosaic virus-infected plants. The Whitefly, *Bemisia tabaci* (Homoptera: Aleyrodidae) Interaction with Geminivirus-Infected Host Plants. Netherlands: Springer; 2011, 107-119.
- [17]. Colvin J, Omongo CA, Govindappa MR, Stevenson PC, Maruthi MN, Gibson G, Seal SE, Muniyappa V: Host-plant viral infection effects on arthropod-vector population growth, development and behaviour: management and epidemiological implications. *Adv Virus Res* 2006, 67:419-452. 21.
- [18]. Legg JP, Sseruwagi P, Boniface S, Okao-Okuja G, Shirima R, Bigirimana S, Gashaka G, Herrmann HW, Jeremiah S, Obiero H: Spatio-temporal patterns of genetic change amongst populations of cassava *Bemisia tabaci* whiteflies driving virus pandemics in East and Central Africa. *Virus Res* 2014, 186:61-
- [19]. Boykin LM, Kinene T, Wainaina JM, Savill A, Seal S, Mugerwa H, Macfadyen S, Tay WT, De Barro P, Kubatko L: Review and guide to a future naming system of African *Bemisia tabaci* species. *Syst Entomol* 2018, 43:427-433.
- [20]. Ateka E, Alicai T, Ndunguru J, Tairo F, Sseruwagi P, Kiarie S, Makori T, Kehoe MA, Boykin LM: Unusual occurrence of a DAG motif in the Ipomovirus cassava brown streak virus and implications for its vector transmission. *PLoS One* 2017, 12e0187883.
- [21]. Bedford ID, Markham PG, Brown JK, Rosell RC: Geminivirus transmission and biological characterisation of whitefly (*Bemisia tabaci*) types from different geographic regions. *Ann Appl Biol* 1994, 125:311-325.
- [22]. Maruthi MN, Colvin J, Seal S, Gibson G, Cooper J: Co-adaptation between cassava mosaic geminiviruses and their local vector populations. *Virus Res* 2002, 86:71-85.
- [23]. Szyniszewska AM, Busungu C, Boni SB, Shirima R, Bouwmeester H, Legg JP: Spatial analysis of temporal changes in the pandemic of severe cassava mosaic disease in Northwestern Tanzania. *Phytopathology* 2017, 107:1229-1242.
- [24]. Ghosh S, Bouvaine S, Richardson SCW, Ghanim M, Maruthi MN: Fitness costs associated with infections of secondary endosymbionts in the cassava whitefly species *Bemisia tabaci*. *J Pest Sci (2004)* 2018, 91:17-28.
- [25]. Njoroge MK, Mutisya D, Milano D, Kilalo D: Whitefly species efficiency in transmitting cassava mosaic and brown streak diseases. *Cogent Biol* 2017, 3:1-8 1311499.
- [26]. Dinsdale A, Cook L, Riginos C, Buckley YM, De Barro AP: Refined global analysis of *Bemisia tabaci* (Hemiptera: Sternorrhyncha: Aleyrodoidea: Aleyrodidae) mitochondrial cytochrome oxidase 1 to identify species level genetic boundaries. *Ann Entomol Soc Am* 2010, 103:196-208.
- [27]. Boykin LM: *Bemisia tabaci* nomenclature: lessons learned. *Pest Manag Sci* 2014, 70:1454-1459.
- [28]. Boykin LM, Savill A, De Barro P: Updated mtCOI reference dataset for the *Bemisia tabaci* species complex. *F1000Research* 2017, 6:1835.
- [29]. Elfekih S, Tay WT, Gordon K, Court LN, De Barro PJ: Standardized molecular diagnostic tool for the identification of cryptic species within the *Bemisia tabaci* complex. *Pest Manag Sci* 2018, 74:170-173.
- [30]. Mugerwa H, Seal S, Wang H-L, Patel MV, Kabaalu R, Omongo CA, Alicai T, Tairo F, Ndunguru J, Sseruwagi P: African ancestry of new world, *Bemisia tabaci*-whitefly species. *Sci Rep* 2018, 8:1- 11.
- [31]. Brown JK, Idris AM: Genetic differentiation of whitefly *Bemisia tabaci* mitochondrial cytochrome oxidase i, and phylogeographic concordance with the coat protein of the plant virus genus begomovirus. *Ann Entomol Soc Am* 2005, 98:827-837.
- [32]. Paredes-Montero JR, Haq QI, Mohamed AA, Brown JK. Phylogeographic and SNPs analyses of *Bemisia tabaci* B mitotype populations reveal only two of eight haplotypes are invasive. *Biology*. 2021 Oct 15;10(10):1048.
- [33]. Romba R, Gnankine´ O: Comparative biology parameters of Q1 and Q3 genotypes of *Bemisia tabaci* MED (Hemiptera: Aleyrodidae) on two host plants in Burkina Faso, West Africa. *Afr Entomol* 2018, 26:1-8.
- [34]. Elfekih S, Etter P, Tay WT, Fumagalli M, Gordon K, Johnson E, De Barro P: Genome-wide analyses of the *Bemisia tabaci* species complex reveal contrasting patterns of admixture and complex demographic histories. *PLoS One* 2018, 13:1-18.

- [35]. Tajebe LS, Boni SB, Guastella D, Cavalieri V, Lund OS, Rugumamu CP, Rapisarda C, Legg JP: Abundance, diversity and geographic distribution of cassava mosaic disease pandemic associated *Bemisia tabaci* in Tanzania. *J Appl Entomol* 2015, 139:627-637.
- [36]. Chen W, Hasegawa DK, Kaur N, Kliot A, Pinheiro PV, Luan J, Stensmyr MC, Zheng Y, Liu W, Sun H: The draft genome of whitefly *Bemisia tabaci* MEAM1, a global crop pest, provides novel insights into virus transmission, host adaptation, and insecticide resistance. *BMC Biol* 2016, 14:1-15.
- [37]. Sseruwagi P, Wainaina J, Ndunguru J, Tumuhimbise R, Tairo F, Guo J-Y, Vrieling A, Blythe A, Kinene T, De Marchi B: The first transcriptomes from field-collected individual whiteflies (*Bemisia tabaci*, Hemiptera: Aleyrodidae). *Gates Open Res* 2017, 1:16.
- [38]. Wosula EN, Chen W, Fei Z, Legg JP: Unravelling the genetic diversity among cassava *Bemisia tabaci* whiteflies using NextRAD sequencing. *Genome Biol Evol* 2017, 9:2958-2973.
- [39]. Clark MA, Baumann L, Munson MA, Baumann P, Campbell BC, Duffus JE, Osborne LS, Moran NA: The eubacterial endosymbionts of whiteflies (Homoptera: Aleyrodoidea) constitute a lineage distinct from the endosymbionts of aphids and mealybugs. *Curr Microbiol* 1992, 25:119-123.
- [40]. Baumann L, Thao ML, Funk CJ, Ng JCK, Baumann P, Falk BW: Sequence analysis of DNA fragments from the genome of the primary endosymbiont of the whitefly *Bemisia tabaci*. *Curr Microbiol* 2004, 48:77-81.
- [41]. Thao ML, Baumann P: Evolutionary relationships of primary prokaryotic endosymbionts of whiteflies and their hosts. *Appl Environ Microbiol* 2004, 70:3401-3406.
- [42]. Thierry M, Becker N, Hajri A, Reynaud B, Lett J-M, Delatte H: Symbiont diversity and non-random hybridization among indigenous (Ms) and invasive (B) biotypes of *Bemisia tabaci*. *Mol Ecol* 2011, 20:2172-2187.
- [43]. Ghosh S, Bouvaine S, Maruthi MN: Prevalence and genetic diversity of endosymbiotic bacteria infecting cassava whiteflies in Africa. *BMC Microbiol* 2015, 15:93.
- [44]. Gnankine O, Mouton L, Henri H, Terraz G, Houndete T, Martin T, Vavre F, Fleury F: Distribution of *Bemisia tabaci* (Homoptera: Aleyrodidae) biotypes and their associated symbiotic bacteria on host plants in West Africa. *Insect Conserv Divers* 2013, 6:411-421.
- [45]. Mauck KE: Variation in virus effects on host plant phenotypes and insect vector behavior: what can it teach us about virus evolution? *Curr Opin Virol* 2016, 21:114-123.
- [46]. Wei J, He Y-Z, Guo Q, Guo T, Liu Y-Q, Zhou X-P, Liu S-S, Wang XW, Raikhel AS: Vector development and vitellogenin determine the transovarial transmission of begomoviruses. *Proc Natl Acad Sci U S A* 2017, 114:6746-6751.
- [47]. Khan, A. J., Mansoor, S., & Briddon, R. W. (2014). Oman: a case for a sink of begomoviruses of geographically diverse origins. *Trends in plant science*, 19(2), 67-70.
- [48]. Khan, A. J., Akhtar, S., Al-Matrushi, A. M., Fauquet, C. M., & Briddon, R. (2013a). Introduction of East African cassava mosaic Zanzibar virus to Oman harks back to "Zanzibar, the capital of Oman." *Virus g."es*, 46(1), 195-198.
- [49]. Khan, A. J., Akhtar, S., Al-Zaidi, A. M., Singh, A. K., & Briddon, R. W. (2013b). Genetic diversity and distribution of a distinct strain of Chili leaf curl virus and associated betasatellite infecting tomato and pepper in Oman. *Virus research*, 177(1), 87-97.
- [50]. Khan, A. J., Akhtar, S., Briddon, R. W., Ammara, U., Al-Matrooshi, A. M., & Mansoor, S. (2012). Complete nucleotide sequence of watermelon chlorotic stunt virus originating from Oman. *Viruses*, 4(7), 1169-1181.
- [51]. Haq, Q. M. I., & Sohrab, S. S. (2020). Begomovirus research in Oman: a critical appraisal and the way ahead. In *Applied Plant Virology* (pp. 455-460). Academic Press.
- [52]. Khan, A. J., Idris, A. M., Al-Saady, N. A., Al-Mahruki, M. S., Al-Subhi, A. M., & Brown, J. K. (2008). A divergent isolate of Tomato yellow leaf curl virus from Oman with an associated DNA β satellite: an evolutionary link between Asian and the Middle Eastern virus-satellite complexes. *Virus Genes*, 36(1), 169-176.
- [53]. Avidov, Z. Bionomics of the tobacco whitefly (*Bemisia tabaci* Gennad.) in Israel. *Ktavim* 1956, 7, 25-41.
- [54]. Brown, J.K. Whitefly-transmitted geminiviruses and associated disorders in the Americas and the Caribbean basin. *Plant Dis.* 1992, 76, 220. [CrossRef]
- [55]. Bedford, I.D.; Briddon, R.W.; Brown, J.K.; Rosell, R.C.; Markham, P.G. Geminivirus transmission and biological characterization of *Bemisia tabaci* (Gennadius) biotypes from different geographic regions. *Ann. Appl. Biol.* 1994, 125, 311-325. [CrossRef]
- [56]. Jones, D.R. Plant viruses transmitted by whiteflies. *Eur. J. Plant Pathol.* 2003, 109, 195-219. [CrossRef]
- [57]. Azab, A.K.; Megahed, M.M.; E1-Mirsawi, D.H. On the biology of *Bemisia tabaci* (Genn.) [Homoptera—Homoptera: Aleyrodidae]. *Bull. Soc. Entomol. Egypt* 1971, 4, 305-315.
- [58]. Horowitz, A.; Podoler, H.; Gerling, D. Life table analysis of the tobacco whitefly *Bemisia tabaci* (Gennadius) in cotton fields in Israel. *Acta Oecologica Oecologia Appl. Fr.* 1984, 5, 221-233.
- [59]. Gerling, D.; Horowitz, A.; Baumgaertner, J. Autecology of *Bemisia tabaci*. *Agric. Ecosyst. Environ.* 1986, 17, 5-19. [CrossRef]
- [60]. Brown, J.K. Phylogenetic biology of the *Bemisia tabaci* sibling species group. In *Bemisia: Bionomics and Management of a Global Pest*; Stansly, P.A., Naranjo, S.E., Eds.; Springer: Dordrecht, The Netherlands, 2010;

- pp. 31–67, ISBN 978-90-481-2460-2.
- [61]. Bayhan, E.; Ulusoy, M.R.; Brown, J.K. Host range, distribution, and natural enemies of *Bemisia tabaci* 'B biotype' (Hemiptera: Aleyrodidae) in Turkey. *J. Pest Sci.* 2006, 79, 233–240. [CrossRef]
- [62]. Paredes-Montero, J.R.; Ibarra, M.A.; Arias-Zambrano, M.; Peralta, E.L.; Brown, J.K. Phylo-biogeographical distribution of whitefly *Bemisia tabaci* (Insecta: Aleyrodidae) mitotypes in Ecuador. *Ecosphere* 2020, 11, 1–20. [CrossRef]
- [63]. Shaurub, E.S.H.; Paredes-Montero, J.R.; Brown, J.K.; Zein, H.S.; Mohamed, A.A. Metabolic resistance to organophosphate insecticides in natural populations of the whitefly *Bemisia tabaci* (Hemiptera: Aleyrodidae) in Egypt and molecular identification of mitotypes. *Phytoparasitica* 2021, 49, 443–457. [CrossRef]
- [64]. Rekha, A.; Maruthi, M.; Muniyappa, V.; Colvin, J. Occurrence of three genotypic clusters of *Bemisia tabaci* and the rapid spread of the B biotype in south India. *Entomol. Exp. Appl.* 2005, 117, 221–233. [CrossRef]
- [65]. Legg, J.P.; Sseruwagi, P.; Boniface, S.; Okao-Okuja, G.; Shirima, R.; Bigirimana, S.; Gashaka, G.; Herrmann, H.-W.; Jeremiah, S.; Obiero, H.; et al. Spatio-temporal patterns of genetic change amongst populations of cassava *Bemisia tabaci* whiteflies driving virus pandemics in East and Central Africa. *Virus Res.* 2014, 186, 61–75. [CrossRef] [PubMed]
- [66]. Castro, J.A.; Picornell, A.; Ramon, M. Mitochondrial DNA: A tool for populational genetics studies. *Int. Microbiol.* 1998, 1, 327–332.
- [67]. De Moya, R.S.; Brown, J.K.; Sweet, A.D.; Walden, K.K.O.; Paredes-Montero, J.R.; Waterhouse, R.M.; Johnson, K.P. Nuclear orthologs derived from whole genome sequencing indicate cryptic diversity in the *Bemisia tabaci* (Insecta: Aleyrodidae) complex of Whiteflies. *Diversity* 2019, 11, 151. [CrossRef]
- [68]. Brown, J.K.; Frohlich, D.R.; Rosell, R.C. The sweetpotato or silverleaf whiteflies: Biotypes of *Bemisia tabaci* or a species complex? *Annu. Rev. Entomol.* 1995, 40, 511–534. [CrossRef]
- [69]. Delatte, H.; Reynaud, B.; Granier, M.; Thornary, L.; Lett, J.; Goldbach, R.; Peterschmitt, M. A new silverleaf-inducing biotype Ms of *Bemisia tabaci* (Hemiptera: Aleyrodidae) indigenous to the islands of the south-west Indian Ocean. *Bull. Entomol. Res.* 2005, 95, 29–35.

DOI: <https://doi.org/10.15379/ijmst.v10i1.2611>

This is an open access article licensed under the terms of the Creative Commons Attribution Non-Commercial License (<http://creativecommons.org/licenses/by-nc/3.0/>), which permits unrestricted, non-commercial use, distribution and reproduction in any medium, provided the work is properly cited.